IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Appellants: Maura C. Cannon, Francis C. Cannon, Gabriel J. McCool, Henry E. Valentin, and Kenneth J. Gruys

Serial No.:	09/479,040	Art Unit:	1634
Filed:	January 7, 2000	Examiner:	A. Chakrabarti

For: *"POLYHYDROXYALKANOATE BIOSYNTHESIS ASSOCIATED PROTEINS AND CODING REGION IN BACILLUS MEGATERIUM"*

Assistant Commissioner for Patents
Washington, D.C. 20231

APPEAL BRIEF

Sir:

This is an appeal from the final rejection of claims 1-6, 9, 11-14, 24 and 25 in the Office Action mailed July 26, 2002, in the above-identified patent application. A Notice of Appeal was mailed on January 24, 2003. A check in the amount of $215.00 for the filing of this Appeal Brief and a one month extension of time, up to and including April 24, 2003, for a small entity are also enclosed. It is believed that no additional fee is required with this submission. However, should an additional fee be required, the Commissioner is hereby authorized to charge the fee to Deposit Account No. 50-1868.

(1) REAL PARTY IN INTEREST

The real party in interest of this application is the assignee University of Massachusetts, Amherst, MA, and the licensee Metabolix, Inc., Cambridge, MA.

(2) RELATED APPEALS AND INTERFERENCES

There are no related appeals or interferences known to appellant, the undersigned, or appellant's assignee which directly affects, which would be directly affected by, or which would have a bearing on the Board's decision in this appeal.

(3) STATUS OF CLAIMS ON APPEAL

Claims 1, 3-6, 9, 11-14, 24 and 25 are pending and on appeal. The text of each claim on appeal, as pending, is set forth in an Appendix to this Appeal Brief.

(4) STATUS OF AMENDMENTS

The claims were last amended in the Amendment mailed July 11, 2002.

(5) SUMMARY OF THE INVENTION

Appellants have cloned from a bacteria, *Bacillus megaterium*, the gene encoding a bacterial enzyme, a 3-keto-acyl-CoA reductase (page 60, line 20 to page 61, line 2). The gene encoding the enzyme can be introduced into other bacteria for use in synthesis of polyhydroxyalkanoates (PHAs) (page 61, line 6 to page 62). The enzyme isolated from *Bacillus* megaterium has low homology to reductases isolated from other bacteria, and has a significant difference in molecular weight from the most studied reductase used for PHA synthesis, the reductase from *P. oleovarans* (a difference between 362 amino acids as compared to 636 amino acids) (page 54, lines 7-17). The most striking feature of the reductase is its substrate specificity, being specific for the D-stereoisomer of C6 enoyl-CoA esters (page 60, line 20 to page 61, line 5).

The claimed compositions are directed to isolated or purified nucleic acid segments; recombinant vectors (see claim 3 as originally filed); and recombinant cells; comprising a nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein (claim 1, as originally filed), wherein the nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:8 (claim 1, as originally filed) that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof (claim 1, as originally filed), and encodes a protein at least about 80% identical to SEQ ID NO:9 (claim 1, as originally filed) and has 3-keto-acyl-CoA reductase activity higher for D-isomers of C6 carbon chains than for C4 carbon chains (Table 6, page 61 of specification). The recombinant vector also comprises a 3' transcription terminator (see claim 3 as originally filed).

The compositions are also directed to a genetically transformed plant or cell (page 36, line 20 to page 37, line 11; claims 5 and 6 as originally filed), comprising in the 5' to 3' direction: a promoter that directs transcription of a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein; wherein the structural nucleic acid sequence has at least about 80% identical to SEQ ID NO:8 that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof; and encodes a protein at least 80% identical to SEQ ID NO:9 and that has 3-keto-acyl-CoA reductase activity higher for D-isomers of C6 carbon chains than for C4 carbon chains; a 3' transcription terminator; and a 3' polyadenylation signal sequence that directs the addition of polyadenylate nucleotides to the 3' end of RNA transcribed from the structural nucleic acid sequence (claims 5 and 6 as originally filed). The compositions are also directed to an isolated or purified nucleic acid segment (claims as originally filed, and page 11, line 5); a

recombinant vector (claim 11 as originally filed); and recombinant host cells (claim 12 as originally filed); comprising a nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein, wherein the nucleic acid segment is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity. The recombinant vector also comprises a 3' transcription terminator. The compositions are also directed to a genetically transformed plant (claim 14 as originally filed); and a genetically transformed plant cell (claim 13 as originally filed), comprising in the 5' to 3' direction: a promoter that directs transcription of a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity; a 3' transcription terminator; and a 3' polyadenylation signal sequence that directs the addition of polyadenylate nucleotides to the 3' end of RNA transcribed from the structural nucleic acid sequence. The compositions are also directed to nucleic acid segments, vectors, or cells comprising the nucleic acid sequence SEQ ID NO:8 (see pages 27-32). Lastly, the compositions are directed to nucleic acid segments, vectors, or cells comprising the nucleic acid sequence SEQ ID NO:10 (see pages 33-37).

(6) ISSUES ON APPEAL

The issues presented on appeal are:

(1) whether claims 1, 3-6, 9, 11-14 and 24-25 fail to comply with the written description requirement under 35 U.S.C. § 112, first paragraph.

(7) GROUPING OF CLAIMS

The claims do not stand or fall together. The claims can be grouped as follows: (1) claims 1, 3-6, 9, and 11-14, and (2) claims 24 and 25. Claims 1, 3-6, 9, and 11-14 are directed, in part, to compositions comprising structural nucleic acid sequences encoding a polyhydroxyalkanoate synthase protein, or a 3-keto-acyl-CoA reductase protein, wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10, or SEQ ID NO:8, respectively, and hybridizes under stringent conditions to SEQ ID NO:10, or SEQ ID NO:8, or the complements thereof. Claims 24 and 25 are directed to compositions comprising isolated or purified nucleic acid segments, vectors, or cells harboring SEQ ID NOs. 8 or SEQ ID NO:10. Reasons for this grouping and arguments for the separate patentability of these groups of claims are provided below.

(8) ARGUMENTS

(a) The Claimed Invention

In the late 1980's, the bacterial enzymes essential for production of polyhydroxyalkanoates in bacteria or transgenic plants were cloned and then introduced into another bacterial host nor naturally producing polyhydroxyalkanoates, and shown to produce polyhydroxybutyrate. There are three essential enzymes, which act sequentially on substrate to produce the final product: (1) a beta-ketothiolase (PhaA) which condenses two molecules of acetyl CoA, (2) a stereo-specific reduction catalyzed by an NADPH dependent acetoacetyl-CoA

reductase (PhaB), and (3) a PHA synthase (PhaC) which polymerizes the monomers to produce the polyalkanoate. The first enzymes were cloned from *Alcaligenes eutrophus*, and were able only to produce polyhydroxybutyrate. Subsequently, a PHA synthase was isolated from *Pseudomonas oleovarans* which was effective on longer carbon chain substrates, and other polyhydroxyalkanoates could be produced. By the time this application had been filed, enzymes had been isolated from over twenty different types of bacterial, in the hopes of identifying enzymes with different substrate specificity, to provide a means of making additional polyhydroxyalkanoates by genetic engineering of bacteria and plants, since the properties of the polyhydroxyalkanoates vary greatly depending upon their composition.

The claimed invention is based on the cloning of a 3-keto-acetyl-CoA cDNA found in a particularly type of bacteria, *Bacillus megaterium.* This enzyme is characterized by a D-specific reduction primarily of C6 substrates. The claims are directed to isolated or purified nucleic acid segments predicated on their ability to hybridize under stringent conditions to already isolated nucleic acid targets. For example, an isolated nucleic acid sequence comprising a sequence encoding a 3-keto-acyl-CoA reductase protein, wherein the sequence hybridizes to SEQ ID NO:8 or the complement thereof, and encodes a protein at least about 80% identical to SEQ ID NO:9, and has 3-keto-acyl-CoA reductase activity higher for D-isomers of C6 carbon chains than for C4 carbon chains. As will be discussed below, the functionality of the protein encoded by the nucleic acid, in combination with the defined structural features dictated by hybridization to a target sequence, clearly convey that the Appellants are in possession of the claimed compositions.

There are a total of two *nucleic acid* sequences to which the claimed compositions rely upon to provide distinguishing structural features for the compositions of claims 1, 3, 4, 5, 6, 9, 11, 12, 13 and 14 (SEQ ID NO:8 and SEQ ID NO:10). There are a total of two *protein* sequences to which the claimed compositions rely upon to further provide distinguishing structural features to the compositions of claims 1, 3, 4, 5, 6, 9 and 11-14 (SEQ ID NO:9 and SEQ ID NO:11).

The claimed invention is *specifically* directed to isolated or purified nucleic acid segments, vectors, or cells harboring SEQ ID NO:8 or SEQ ID NO:10 (Claims 24 and 25). Claim 24 is directed to the nucleic acid segment, vector, or cell of preceding claims 1, 4, 5, or 6, wherein the nucleic acid sequence ***is*** SEQ ID NO:8. Claim 25 is directed to the nucleic acid segment acid segment, vector, or cell of preceding claims 9, 11, 12, 13, or 14 wherein the nucleic acid sequence ***is*** SEQ ID NO:10.

(b) Rejections Under 35 U.S.C. § 112

i. The Legal Standard for Written Description

Both the written description and enablement requirements are defined by 35 U.S.C. § 112, first paragraph, which states that the patent specification must contain "a written description of the invention, and of the manner and process of making and using it...[such] as to enable any person of ordinary skill in the art to which it pertains ... to make and use the same ... " The purpose of the written description requirement is to prevent a patentee from later asserting that he invented something which he did not. Thus the patentee must "recount his invention in such detail that his future claims can be determined to be encompassed within his original creation."

Vas- Cath Inc. v. Mahurkar, 935 F.2d 1555, 1561, 19 U.S.P.Q.2d 1111, 1115 (Fed. Cit 1991). The purpose of the enablement requirement is to teach those of ordinary skill in the art how to make and use the invention without "undue experimentation." The specification does not need to teach what is already known in the art. The specification is enabled if one of ordinary skill in the art only engages in routine experimentation to make the invention.

For many years the leading case for the written description requirement in the biotechnology and pharmaceutical arts was *Eli Lilly v. Univ. of Calif. Board of Regents* In *Regents of University of California v. Eli Lilly & Co.*, 119 F.3d 1559, 43 U.S.P.Q.2d 1398 (Fed. Cir. 1997), *cert denied*, 523 U.S. 1089 (1998). The Federal Circuit evaluated whether claims to recombinant production of human insulin in U.S. Patent No. 4,652,525 (herein referred to as "the '525 patent") met the written description requirement. The court determined that the specification failed to comply with the written description requirement for only disclosing a single species of DNA encoding non-human insulin.

In *Enzo Biochem*, the Federal Circuit held that that the written description requirement can be met by a functional description of claimed materials, if coupled with a known or disclosed correlation between function and structure. *Enzo Biochem, Inc., v. Gen-Probe, Inc.*, 296 F.3d 1316, 63 U.S.P.Q.2d 1609 (Fed. Cir.2002) ("*Enzo II*"). The Federal Circuit held that a patentee complied with the written description requirement by depositing biological material in a public depository. The specification described the nucleotide sequence in terms of its ability to bind to *N. gonorrhoeae*. The patent had issued with no written description rejection. Nevertheless, the Federal Circuit had determined in *Enzo I* that, because the inventor had not described the actual

nucleotide sequence of the probes in the patent specification, the written description was inadequate as a matter of law. In *Enzo II*, the Federal Circuit rejected its narrow interpretation of *Eli Lilly* that the disclosure of the sequence was always necessary, and instead adopted a broader interpretation of the types of disclosures that comply with the written description requirement. The court adopted provisions from the Guidelines issued by the U.S. Patent and Trademark Office that state that the written description requirement can be met by a functional description of claimed materials, if coupled with a known or disclosed correlation between function and structure. The court found that the written description requirement was met when, in the knowledge of the art, the disclosed function is sufficiently correlated to a particular, known structure.

This standard has been reviewed and clarified further in the recent decision of *Amgen Inc. v. Hoechst Marion Roussel, Inc. and Transkaryotic Therapies, Inc.* 314 F.3d 1313, 65 USPQ 2d (Fed. Cir. 2003). This decision was the appeal of a lengthy district court ruling on validity, infringement, and enforceability of five Amgen patents relating to production of erythropoietin (EPO), a hormone that controls formation of red blood cells. Amgen's EPO is sold under the brand name EPOGEN®. Amgen asserted that Hoechst (now Aventis Pharmaceuticals, Inc.) and Transkaryotic Therapies ("TKT") infringed U.S. Patent No. 5,547,933; 5,618,698; 5,621,080; 5,756,349; and 5,955,422, due to the filing of TKT's Investigational New Drug Application (INDA). All of the patents shared the same disclosure. TKT recombinantly produced EPO using a method that differed from the method used by Amgen and described in the patents. TKT

inserted a promoter which caused the expression of ordinarily unexpressed endogenous (or "native") EPO DNA in human cells to produce the EPO.

The Federal Circuit upheld the lower court's claim construction and its decision that the claims comply with the written description and enablement requirements of 35 U.S.C. § 112. In rendering its decision, the Court continued in the manner of *Enzo II* and applied a broad interpretation of the types of disclosures that comply with the written description requirement. TKT asserted that claims did not meet the written description requirement since Amgen had failed to describe the use of all mammalian and vertebrate cells, relying on the earlier *Lilly* decision.

Relying heavily on the expert testimony provided in the District Court proceeding, the Federal Circuit held that this description adequately supports the claims covering EPO made using the genus vertebrate or mammalian cells.

One question that arose out of these proceedings was whether or not Amgen's disclosure of one means of producing synthetic EPO in mammalian cells, namely exogenous DNA expression, entitles it to claim all EPO produced by mammalian cells in culture, or all cultures vertebrate cells that produce EPO. The district court in this case found that "the specification need teach only one mode of making and using a claimed composition." *Amgen, Inc v. Hoechst Marion Roussel, Inc* 126 F.Supp.2d 69, 160, 57 USPQ 2d 1449, 1515 (D.Mass.2001).

ii. Claims 1, 3-6, 9, 11-14, and 24-25 were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a

way as to reasonably convey that the inventor had possession of the claimed invention at the time of filing.

The specification teaches what the claimed compounds are and how to use them. The written description requirement can be met by "show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics...i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." Guidelines, 66 Fed. Reg. at 1106 (emphasis added). It is well established in the art of nucleic acid research that a very strong correlation exists between *nucleic acid structure* and *hybridization of the nucleic acid to a known target*. In the presently claimed compositions, knowing the nucleic acid structures is predicated upon hybridizing to the *known* target sequence. The claimed compositions are required to 1) be at least about 80% identical to SEQ ID NO:8 or SEQ ID NO:10, and 2) hybridize under stringent conditions to SEQ ID NO:8, or SEQ ID NO:10, or the complement thereof. The appellants submit that hybridizing under stringent conditions to SEQ ID NO:8, or SEQ ID NO:10, *is not an intended use*, but rather an inherent property of the claimed sequence(s). This inherent property *does* modify the claimed product, because it distinguishes those presently claimed sequences from sequences that are not complementary to the target under stringent conditions, and it paints a clear mental picture of base pair interactions at the molecular level. This complementary/hybridizing property defines structural features that can only be common to the claimed genus of sequences. The claimed sequences inherently *hybridize* (i.e. the claims are not method claims for screening hybridizing sequences), and

therefore structural features, such as correct charge and spatial orientation of the hydrogen bond donors acceptors that provide a specific binding surface for the target, are known; *especially in view of the 80% identical nature of the nucleic acid bases*. One of ordinary skill in the art will readily appreciate that the arrangement of donor and acceptor sites: 1) distinguish any binding sequence from non-binding sequences; 2) are an inherent feature of all nucleic acid sequences (it is their order and spatial orientation that is the distinguishing hallmark of complementation/hybridization); and, in the case of screening for nucleic acids that fall with the scope of the claimed invention, 3) readily allow one of ordinary skill in the art to make a determination as to whether the sequences harbor hydrogen bond donor and acceptor sites in the proper orientation. The three foregoing tenets define the structure of nucleic acid segments. All of these features are well known in the art, and were known well before the filing date of the present application. The art has established a strong correlation between nucleic acid structure and hybridization. One skilled in the art would be able to predict with a reasonable degree of confidence the structure of the claimed compositions from a recitation of "hybridization" to SEQ ID NO:8 or SEQ ID NO:10. Whether or not the claimed nucleic acid segments harbor 80%, 90%, or 99% identity to SEQ ID NO:8, determination as to the structure, and in particular the structure surrounding those bases that are not identical, is based upon the ability of the claimed nucleic acids to hybridize to SEQ ID NO:8, under stringent conditions.

The common elements and attributes (i.e. structure) are defined by the features that govern hybridization (i.e. well known molecular forces at the interface between a nucleic acid and a target). One of ordinary skill in the are inherent to all nucleic acid sequences. The

question is whether, or not, these features are properly orientated to govern binding to the target nucleic acid, thereby defining structure. These features are properly orientated in the claimed nucleic acids. The *method* of isolation (hybridization) is predicated on structure.

Furthermore, the appellants respectfully submit that claims 24 and 25 are *specifically* directed to isolated or purified nucleic acid segments, vectors, or cells harboring SEQ ID NOs. 8 or SEQ ID NO:10 (Claims 24 and 25). Claim 24 is directed to the nucleic acid segment, vector, or cell of preceding claims 1, 4, 5, or 6, wherein the nucleic acid sequence ***is*** SEQ ID NO:8. Claim 25 is directed to the nucleic acid segment acid segment, vector, or cell of preceding claims 9, 11, 12, 13, or 14 wherein the nucleic acid sequence ***is*** SEQ ID NO:10. There should not be any argument as to the structure of the claimed nucleic acid sequences of claims 24 and 25. Claims 24 and 25 do NOT encompass nucleic acid sequences different from those disclosed as SEQ ID NOs.8 and 10, respectively.

iii. Claims 1, 3-6, 9, and 11-14 were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey that the inventor had possession of the claimed invention at the time of filing.

The appellants respectfully submit that the compositions (for example, claims 1, 4, 9, and 12) are directed to isolated or purified nucleic acid segments that hybridize to an isolated target sequence. One of ordinary skill in the art can readily envision the detailed chemical structure of the claimed DNA sequences encoding for the proteins. The targets (SEQ ID NO:8 and SEQ ID NO:10) in combination with known hybridization methods provide a clear picture of the claimed structures.

The appellants respectfully submit that the number of claimed sequences are defined by the limits of hybridization *methods used* to isolate the claimed nucleic acids. The target nucleic acids (SEQ ID NO:8 or SEQ ID NO:10) put a limit on the number, and types, of common attributes or features shared by the claimed members. Furthermore, the functional limitation, wherein the sequence encodes a 3-keto-acyl-CoA reductase protein, or a polyhydroxyalkanoate synthase protein, further defines the inherent features of the claimed compositions. The target nucleic acid, which has already been identified, is the "rate-limiting" component in a hybridization assay. It is the "lock" that can only be accessed by the "key" (the nucleic acid exhibiting about 80% homology). The *inherent ability* of the claimed nucleic acid to hybridize extends beyond functional utility; it defines the chemical and structural makeup of the binding sequence.

(c) The Examiner has failed to individually examine the dependent claims.

It is well established that each claim must be separately examined for patentability. It is not enough here to look at a single independent claim and reject all claims. No rationale has been presented as to why there is a lack of written description for the subject matter of claims 24 and 25, wherein the nucleic acid segment ***is*** SEQ ID NO:8 or SEQ ID NO:10, respectively. The Examiner has stated only claims limited to the disclosed sequences are patentable under 35 U.S.C. § 112 (see page 3 of the Office Action mailed on October 23, 2001).

(9) SUMMARY AND CONCLUSION

An understanding of nucleic acid structure is the result of a detailed analysis of the molecular interactions between the claimed nucleic acid and its target nucleic acid (i.e. the

hydrogen bonding arrangements and hydrophobic interactions between sequences that hybridize to one another). One of skill in the art will recognize that, in view of the present specification, the identification and characterization of the target nucleic acid sequences (SEQ ID NO:8 and SEQ ID NO:10) actually dictates and defines the specific conformation and the "order" of complementary groups on the claimed nucleic acids that must be assembled in order to recognize the "target" region.

The formation of a complementary interface between SEQ ID NO:8 or SEQ ID NO:10, and the claimed nucleic acids is based upon, *inter alia*, the recognition of specific and accessible hydrogen bonds. This interface lies at the core of the presently claimed compositions because it precisely defines the nucleic acid for which the target sequences will accept as their "partner(s)".

In summary, the Appellants have described significant structural and physical properties of the claimed nucleic acids and their cognate sequence targets. The specification, in view of what was commonly accepted in the art at the time of filing the present application, is clearly sufficient for one of ordinary skill in the art to realize the appellants are in possession of the claimed nucleic acids.

For the foregoing reasons, Appellant submits that the claims 1, 3-6, 9, 11-14, 24 and 25 are patentable.

Respectfully submitted,

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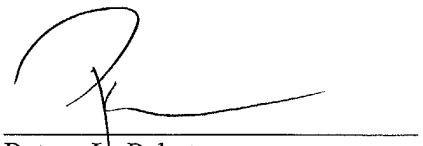

Patrea L. Pabst

Date: April 24, 2003

Appendix: Claims On Appeal

1. (Three Times Amended) An isolated or purified nucleic acid segment comprising a nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein, wherein the nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:8 that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof, and

encodes a protein at least about 80% identical to SEQ ID NO:9, and

has 3-keto-acyl-CoA reductase activity higher for D-isomers of C6 carbon chains than for C4 carbon chains.

3. (Amended) A recombinant vector comprising in the 5' to 3' direction:

a) a promoter that directs transcription of a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein;

b) a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:8; that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:9 and that has 3-keto-acyl-CoA reductase activity higher for for D-isomers of C6 carbon chains than for C4 carbon chains; and

c) a 3' transcription terminator.

4. (Amended) A recombinant cell comprising a nucleic acid segment encoding a 3-keto-acyl-CoA reductase protein, wherein the nucleic acid segment is a nucleic acid sequence at least

about 80% identical to SEQ ID NO:8; that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:9 and that has 3-keto-acyl-CoA reductase activity higher for for D-isomers of C6 carbon chains than for C4 carbon chains.

5. (Amended) A genetically transformed plant cell comprising in the 5' to 3' direction:

a) a promoter that directs transcription of a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein;

b) a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:8 that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:9 and that has 3-keto-acyl-CoA reductase activity higher for for D-isomers of C6 carbon chains than for C4 carbon chains;

c) a 3' transcription terminator; and

d) a 3' polyadenylation signal sequence that directs the addition of polyadenylate nucleotides to the 3' end of RNA transcribed from the structural nucleic acid sequence.

6. (Amended) A genetically transformed plant comprising in the 5' to 3' direction:

a) a promoter that directs transcription of a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein;

b) a structural nucleic acid sequence encoding a 3-keto-acyl-CoA reductase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80%

identical to SEQ ID NO:8 that hybridizes under stringent conditions to SEQ ID NO:8 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:9 and that has 3-keto-acyl-CoA reductase activity higher for for D-isomers of C6 carbon chains than for C4 carbon chains;

c) a 3' transcription terminator; and

d) a 3' polyadenylation signal sequence that directs the addition of polyadenylate nucleotides to the 3' end of RNA transcribed from the structural nucleic acid sequence.

9. (Twice Amended) An isolated or purified nucleic acid segment comprising a nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein, wherein the nucleic acid segment is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity.

11. (Amended) A recombinant vector comprising in the 5' to 3' direction:

a) a promoter that directs transcription of a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein;

b) a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity; and

c) a 3' transcription terminator.

12. (Amended) A recombinant host cell comprising a nucleic acid segment encoding a polyhydroxyalkanoate synthase protein, wherein the nucleic acid segment is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity.

13. (Amended) A genetically transformed plant cell comprising in the 5' to 3' direction:

a) a promoter that directs transcription of a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein;

b) a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity;

c) a 3' transcription terminator; and

d) a 3' polyadenylation signal sequence that directs the addition of polyadenylate nucleotides to the 3' end of RNA transcribed from the structural nucleic acid sequence.

14. (Amended) A genetically transformed plant comprising in the 5' to 3' direction:

a) a promoter that directs transcription of a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein;

b) a structural nucleic acid sequence encoding a polyhydroxyalkanoate synthase protein; wherein the structural nucleic acid sequence is a nucleic acid sequence at least about 80% identical to SEQ ID NO:10 that hybridizes under stringent conditions to SEQ ID NO:10 or the complement thereof; and

encodes a protein at least about 80% identical to SEQ ID NO:11 and that has polyhydroxyalkanoate synthase activity;

c) a 3' transcription terminator; and

d) a 3' polyadenylation signal sequence that directs the addition of polyadenylate nucleotides to the 3' end of RNA transcribed from the structural nucleic acid sequence.

24. (Amended) The nucleic acid segment, vector, or cell of claims 1, 4, 5, or 6, wherein the nucleic acid sequence is SEQ ID NO:8.

25. The nucleic acid segment, vector or cell of claims 9, 11, 12, 13, or 14 wherein the nucleic acid sequence is SEQ ID NO:10.

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